AMENDMENTS

Listing of Claims

The following listing of claims replaces all previous listings or versions thereof:

1-43. (Canceled)

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- 44. (New) A method of assessing protein stability, folding and/or solubility comprising:
 - a) providing a fusion protein comprising (i) a protein of interest and (ii) a first segment of a marker protein, wherein said first segment does not affect the folding or solubility of the protein of interest;
 - b) contacting said fusion protein with a second segment of said marker protein, wherein said second segment is capable of structural complementation with said first segment; and
 - d) determining structural complementation,

wherein a greater degree of structural complementation, as compared to structural complementation observed with appropriate negative controls, indicates stability, proper folding and/or solubility of said protein.

- 45. The method of claim 44, wherein said fusion is C-terminal to said protein of interest.
- 46. The method of claim 44, wherein said fusion is N-terminal to said protein of interest.
- 47. The method of claim 44, wherein said marker protein is selected from the group consisting of a target binding protein, an enzyme, a protein inhibitor, a fluorophore and a chromophore.
- 48. The method of claim 47, wherein said marker protein is a target binding protein.

- 49. The method of claim 48, wherein said target binding protein is ubiquitin.
- 50. The method of claim 47, wherein said marker protein is a chromophore.
- 51. The method of claim 50, wherein said chromophore is green fluorescent protein, blue fluorescent protein, yellow fluorescent protein, luciferase or aquorin.
- 52. The method of claim 47, wherein said marker protein is an enzyme.
- 53. The method of claim 52, wherein said enzyme is β-galactosidase, cytochrome c, chymotrypsin inhibitor, Rnase, phosphoglycerate kinase, invertase, staphylococcal nuclease, thioredoxin C, lactose permease, amino acyl tRNA synthase, and dihydrofolate reductase.
- 54. The method of claim 53, wherein said enzyme is β -galactosidase.
- 55. The method of claim 54, wherein said first segment is the α -peptide of β -galactosidase, and said second segment is the ω -peptide of β -galactosidase.
- 56. The method of claim 44, wherein said protein of interest is Alzheimer's amyloid peptide (Aβ), SOD1, presenillin 1 and 2, α-synuclein, amyloid A, amyloid P, CFTR, transthyretin, amylin, lysozyme, gelsolin, p53, rhodopsin, insulin, insulin receptor, fibrillin, α-ketoacid dehydrogenase, collagen, keratin, PRNP, immunoglobulin light chain, atrial natriuretic peptide, seminal vesicle exocrine protein, β2-microglobulin, PrP, precalcitonin, ataxin 1, ataxin 2, ataxin 3, ataxin 6, ataxin 7, huntingtin, androgen receptor, CREB-binding protein, dentaorubral pallidoluysian atrophy-associated protein, maltose-binding protein, ABC transporter, glutathione S transferase, and thioredoxin.
- 57. The method of claim 44, wherein said negative control utilizes a fusion protein that is improperly folded and/or insoluble.